



SUBSTITUTE SEQUENCE LISTING

<110> Hitz, William
Sebastian, Scott
Grace, John
Streit, Leon

<120> SOYBEAN PLANT PRODUCING SEEDS WITH REDUCED LEVELS OF RAFFINOSE
SACCHARIDES AND PHYTIC ACID

<130> BB1077 US DIV

<140> 10/718,952

<141> 2003-11-21

<150> 10/025,003

<151> 2002-03-11

<150> 09/299,315

<151> 1999-04-26

<150> PCT/US98/06822

<151> 1998-04-07

<150> 08/835,751

<151> 1997-04-08

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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
      35             40             45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
      50             55             60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
      65             70             75             80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
      85             90             95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
     100             105             110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
     115             120             125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
     130             135             140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
     145             150             155             160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
     165             170             175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
     180             185             190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
     195             200             205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
     210             215             220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
     225             230             235             240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg

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Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val	275	280	285
Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly	290	295	300
Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp	305	310	315
Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn	325	330	335
His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe	340	345	350
Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn	355	360	365
Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val	370	375	380
Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp	385	390	395
Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu	405	410	415
His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp	420	425	430
Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu	435	440	445
Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser	450	455	460
Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn	465	470	475
Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys	485	490	495
Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys	500	505	510

<210> 3

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 3

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<210> 4
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonuclotide

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 <211> 1533
 <212> DNA
 <213> Glycine max

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 cagtggattg tcaaacccaa atctgtcaaa tacgaattta aaaccaacat ccatgttcct 180
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 <212> PRT
 <213> Glycine max

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 Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
 20 25 30
 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
 35 40 45

Val	Lys	Tyr	Glu	Phe	Lys	Thr	Asn	Ile	His	Val	Pro	Lys	Leu	Gly	Val	50	55	60	
Met	Leu	Val	Gly	Trp	Gly	Gly	Asn	Asn	Gly	Ser	Thr	Leu	Thr	Gly	Gly	65	70	75	80
Val	Ile	Ala	Asn	Arg	Glu	Gly	Ile	Ser	Trp	Ala	Thr	Lys	Asp	Lys	Ile	85	90	95	
Gln	Gln	Ala	Asn	Tyr	Phe	Gly	Ser	Leu	Thr	Gln	Ala	Ser	Ala	Ile	Arg	100	105	110	
Val	Gly	Ser	Phe	Gln	Gly	Glu	Glu	Ile	Tyr	Ala	Pro	Phe	Lys	Ser	Leu	115	120	125	
Leu	Pro	Met	Val	Asn	Pro	Asp	Asp	Ile	Val	Phe	Gly	Gly	Trp	Asp	Ile	130	135	140	
Ser	Asn	Met	Asn	Leu	Ala	Asp	Ala	Met	Ala	Arg	Ala	Lys	Val	Phe	Asp	145	150	155	160
Ile	Asp	Leu	Gln	Lys	Gln	Leu	Arg	Pro	Tyr	Met	Glu	Ser	Met	Leu	Pro	165	170	175	
Leu	Pro	Gly	Ile	Tyr	Asp	Pro	Asp	Phe	Ile	Ala	Ala	Asn	Gln	Glu	Glu	180	185	190	
Arg	Ala	Asn	Asn	Val	Ile	Lys	Gly	Thr	Lys	Gln	Glu	Gln	Val	Gln	Gln	195	200	205	
Ile	Ile	Lys	Asp	Ile	Lys	Ala	Phe	Lys	Glu	Ala	Thr	Lys	Val	Asp	Lys	210	215	220	
Val	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Ser	Asn	Leu	Val	225	230	235	240
Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ala	Val	Asp	Arg	245	250	255	
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val	260	265	270	
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	275	280	285	
Pro	Gly	Leu	Ile	Asp	Leu	Ala	Ile	Ala	Arg	Asn	Thr	Leu	Ile	Gly	Gly	290	295	300	
Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp	305	310	315	320
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	325	330	335	
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	340	345	350	
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Asn	355	360	365	

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
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 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Asn Arg Ala Met Asp
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 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
 405 410 415
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
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 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
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<210> 7
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

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<210> 8
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 8
 cgtaggggac agcaat 16

<210> 9
 <211> 1533
 <212> DNA
 <213> Glycine max

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<210> 10
 <211> 510
 <212> PRT
 <213> Glycine max

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Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
      20             25             30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
      35             40             45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
      50             55             60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
      65             70             75             80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
      85             90             95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
      100            105            110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
      115            120            125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
      130            135            140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
      145            150            155            160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
      165            170            175

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Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
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 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
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 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
 210 215 220
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
 225 230 235 240
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
 245 250 255
 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
 405 410 415
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
 435 440 445
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
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Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

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<211> 1533
<212> DNA
<213> Glycine max

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<213> Glycine max

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20 25 30
His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45
Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60
Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80
Val Ile Ala Asn Arg Glu Asp Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100 105 110
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130 135 140
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145 150 155 160
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
 165 170 175
 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
 180 185 190
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
 195 200 205
 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
 210 215 220
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
 225 230 235 240
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
 245 250 255
 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
 405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
 435 440 445
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
 485 490 495
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
 500 505 510

<210> 13
 <211> 1533
 <212> DNA
 <213> Glycine max

<400> 13
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 cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca 180
 aaattggggg tgatgcttgt ggggtggggg ggaaacaacg gctctaccct caccggtggt 240
 gttattgcta acagagaggg catttcatgg gctacaaagg acaagattca acaagccaat 300
 tactttggct ccctcaccca agcctcagct attcgagttg gatccttcca gggagaggaa 360
 atctatgccc cattcaagag tctgcttcca atgggttaatc ctgacgacat tgtgtttggg 420
 ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac 480
 atcgatttgc agaagcagtt gaggccttac atggaatcca tggttccact ccccgggaatc 540
 tacgaccggg atttcattgc tgccaaccaaa gaggagcgtg ccaacaacgt gattaagggc 600
 acaaagcaag agcaagttca gcaaatacat aaagacatca aggcgtttta ggaagccacc 660
 aaagtggaca aggtgggtgt cctgtggact gccaacacag agaggtatag caatttggtt 720
 gtaggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag 780
 atttctcctt ccaccttgta tgccattgcc tgtgtgatgg aaaatgttcc tttcattaat 840
 ggaagccctc agaacacttt tgtaccaggg ctgattgatc ttgccatcgc gaggaacact 900
 ttgattgggt gagatgactt caagagtggg cagaccaaaa tgaaatctgt gttggttgat 960
 tttcttgtgg gggctggtat caagccaaca tctatagtta gttacaacca tctgggaaac 1020
 aatgatggta tgaatctctc ggctccacaa accttcgcgt ccaaggaaat ctccaagagc 1080
 aacgttggtg acgatatggt caacagcaat gccatcctct atgagcctgg tgaacatccc 1140
 gaccatgttg ttgttattaa gtatgtgcct tacgtagggg atagcaagag agccatggat 1200
 gagtacactt cagagatatt catgggtgga aagaacacca ttgttttgca caacacatgt 1260
 gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc 1320
 actagaatcc agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct 1380
 accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtgggtgaat 1440
 gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt tggattggcc 1500
 ccagagaata acatgattct cgagtacaag tga 1533

<210> 14
 <211> 510
 <212> PRT
 <213> Glycine max

<400> 14
 Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
 1 5 10 15

Glu	Thr	Glu	Ile	Gln	Ser	Val	Tyr	Asn	Tyr	Glu	Thr	Thr	Glu	Leu	Val	
			20					25					30			
His	Glu	Asn	Arg	Asn	Gly	Thr	Tyr	Gln	Trp	Ile	Val	Lys	Pro	Lys	Ser	
		35					40					45				
Val	Asn	Tyr	Gln	Phe	Lys	Thr	Asn	Thr	His	Val	Pro	Lys	Leu	Gly	Val	
	50					55					60					
Met	Leu	Val	Gly	Trp	Gly	Gly	Asn	Asn	Gly	Ser	Thr	Leu	Thr	Gly	Gly	
	65				70					75					80	
Val	Ile	Ala	Asn	Arg	Glu	Gly	Ile	Ser	Trp	Ala	Thr	Lys	Asp	Lys	Ile	
				85					90					95		
Gln	Gln	Ala	Asn	Tyr	Phe	Gly	Ser	Leu	Thr	Gln	Ala	Ser	Ala	Ile	Arg	
			100					105					110			
Val	Gly	Ser	Phe	Gln	Gly	Glu	Glu	Ile	Tyr	Ala	Pro	Phe	Lys	Ser	Leu	
		115					120					125				
Leu	Pro	Met	Val	Asn	Pro	Asp	Asp	Ile	Val	Phe	Gly	Gly	Trp	Asp	Ile	
	130					135					140					
Ser	Asn	Met	Asn	Leu	Ala	Asp	Ala	Met	Ala	Arg	Ala	Lys	Val	Phe	Asp	
	145				150					155					160	
Ile	Asp	Leu	Gln	Lys	Gln	Leu	Arg	Pro	Tyr	Met	Glu	Ser	Met	Val	Pro	
				165					170					175		
Leu	Pro	Gly	Ile	Tyr	Asp	Pro	Asp	Phe	Ile	Ala	Ala	Asn	Gln	Glu	Glu	
			180					185					190			
Arg	Ala	Asn	Asn	Val	Ile	Lys	Gly	Thr	Lys	Gln	Glu	Gln	Val	Gln	Gln	
		195					200					205				
Ile	Ile	Lys	Asp	Ile	Lys	Ala	Phe	Lys	Glu	Ala	Thr	Lys	Val	Asp	Lys	
	210					215					220					
Val	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Ser	Asn	Leu	Val	
	225				230					235					240	
Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ala	Val	Asp	Arg	
				245					250					255		
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val	
			260					265					270			
Met	Glu	Asn	Val	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	
		275					280					285				
Pro	Gly	Leu	Ile	Asp	Leu	Ala	Ile	Ala	Arg	Asn	Thr	Leu	Ile	Gly	Gly	
	290					295					300					
Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp	
	305				310					315					320	
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	
				325					330					335		

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
 405 410 415
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
 435 440 445
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
 485 490 495
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
 500 505 510

<210> 15

<211> 1533

<212> DNA

<213> Glycine max

<400> 15

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cagtcctgt	acaactacga	aaccaccgaa	cttggttcacg	agaacaggaa	tggcacctat	120
cagtggattg	tcaaacccea	atccgtcaac	taccaattta	aaaccaacac	ccatgttcca	180
aaattggggg	tgatgcttgt	gggttgggg	ggaaacaacg	gctctaccct	caccgggtgt	240
gttattgcta	acagagaggg	catttcatgg	gctacaaagg	acaagattca	acaagccaat	300
tactttggct	ccctcaccca	agcctcagct	attcgagttg	gatccttcca	gggagaggaa	360
atctatgccc	cattcaagag	tctgcttcca	atggttaatc	ctgacgacat	tgtgtttggg	420
ggatgggata	tcagcaacat	gaacctggct	gatgccatgg	ccagggcaaa	ggtgtttgac	480
atcgatttgc	agaagcagtt	gaggccttac	atggaatcca	tggttccact	ccccggaatc	540
tacgaccg	atttcattgc	tgccaaccaa	gaggagcgtg	ccaacaacgt	gattaagggc	600
acaaagcaag	agcaagttca	gcaaatcatc	aaagacatca	aggcgtttta	ggaagccacc	660
aaagtggaca	aggtggttgt	cctgtggact	gccaacacag	agaggtatag	caatttgggt	720
gtaggcctta	atgacaccat	ggagaatctc	ttggctgctg	tggaacagaa	tgaggctgag	780
atttctcctt	ccaccttgta	tgccattgcc	tgtgtgatgg	aaaatgttcc	tttcattaat	840
ggaagccctc	agaacacttt	tgtaccaggg	ctgattgatc	ttgccatcgc	gaggaacact	900
ttgattgggtg	gagatgactt	caagagtgg	cagaccaaaa	tgaaatctgt	gttggttgat	960
tttcttgtgg	gggctggtat	caagccaaca	tctatagtta	gttacaacca	tctgggaaac	1020
aatgatggta	tgaatctctc	ggctccacaa	accttccgct	ccaaggaaat	ctccaagagc	1080
aacgttggtg	acgatatgg	caacagcaat	gccatcctct	atgagcctgg	tgaacatccc	1140
gaccatgttg	ttgttattaa	gtatgtgcct	tacgtagggg	atagcaagag	agccatggat	1200

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gagtacactt cagagatatt catgggtgga aagaacacca ttgttttgca caacacatgt 1260
gaggattccc ttttagctgc tcctattatc ttggacttgg tccttcttgc tgagctgagc 1320
actagaatcc agtttaaagc tgaaaatgag ggaaaattcc actcattcca cccagttgct 1380
accattctca gctatctgac caaggctcct ctggttccac cgggtacacc agtggtgaat 1440
gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt tggattggcc 1500
ccagagaata acatgattct cgagtacaag tga                                     1533

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<210> 16

<211> 510

<212> PRT

<213> Glycine max

<400> 16

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Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
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Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
      20                      25                      30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
      35                      40                      45

Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
      50                      55                      60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
      65                      70                      75                      80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
      85                      90                      95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
     100                      105                      110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
     115                      120                      125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
     130                      135                      140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
     145                      150                      155                      160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
     165                      170                      175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
     180                      185                      190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
     195                      200                      205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
     210                      215                      220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
     225                      230                      235                      240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
     245                      250                      255

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Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
 405 410 415
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
 435 440 445
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
 485 490 495
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
 500 505 510

<210> 17

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: additional sequences of 5' primer

<400> 17

gggaattcca tatg

14

<210> 18
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: start of phaseolin promoter

 <400> 18
 aaggaaaaaa gcggccgc 18

 <210> 19
 <211> 12
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: intervening sequence

 <400> 19
 atagccccc aa 12

 <210> 20
 <211> 12
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: start of phaseolin promoter

 <400> 20
 tggctctttg gt 12